

0070777-000026SEQLIST.txt
SEQUENCE LISTING

<110> Genomine, Inc.
POSTECH FOUNDATION
<120> Novel Phytochrome-interacting protein and a use thereof
<130> OP05-1002
<150> KR10-2004-0013663
<151> 2004-02-27
<160> 26
<170> KopatentIn 1.71
<210> 1
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<212> DNA
<213> Artificial Sequence
<220>
<223> PCR primer

<400> 1
ggatccaaat gtcaggctct aggccgact 29

<210> 2
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<213> Artificial Sequence
<220>
<223> PCR primer

<400> 2
ctcgagctac ttgtttgctg cagcgagttc 30

<210> 3
<211> 1455
<212> DNA
<213> Arabidopsis thaliana

<400> 3
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gaactcaaca gcaacaacgc tgtgtattgg gcaaatcgtg catttgctca cacaaaaactg 120
gaggaatatg gcagtgcata acaggatgca tcgaaggcca ttgaagttga ttcaagatac
tctaagggtt attacaggcg tggtgctgcg tatcttgcca tggaaaatt taaggatgcc 180
ttgaaggact tccaaacaggt aaaaaggctt tctcctaattg accctgatgc cacaagaaag
ctaaaggaat gtgagaaagc agtgatgaaa ctcaaatttg aagaagcaat ctctgtgcc 240
gtatctgaaa ggcgttcagt agctgagtcattgacttcc atacaataga ggttgagcca 300
caatattctg gtgctagaat tgagggagag gaagttacct tagatttgt gaaaacgtatg
atggaggatt ttaagaacca aaaaacatttgcataaaacggatgccttatca aatcgtctt 360
420
480
540
600

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cagactaggc aaatcttgct agcactgcct tctctgttg atataagtgt tccacatggc	660
aaacatatca ctgtttgcgg tgacgttcat ggtcagttct acgatcttct caatatcttt	720
gagcttaatg gcctcccttc ggaggagaac ccataacctat ttaatggcga ctttgtggac	780
agaggctcat tctccgttga gatcatcctc actttgtttg ctttcaagtg catgtgccca	840
tcatccatat atctagccag agaaaccat gaaagcaaga gcatgaacaa aatttatggt	900
tttgagggtg aggttcggtc caagttgagt gaaaaattcg tggatctctt tgctgaagtt	960
ttctgttacc tcccgttggc tcatgttata aatgggaagg tcttcgtggt acatggaggt	1020
ctttcagtg ttgacggcgt gaaactctca gacatcagag ccattgacag attctgtgag	1080
ccaccagagg aaggactaat gtgtgaacta ttgtggagtg atcctaacc tctccctgga	1140
agaggcccaa gcaagcgagg agttggtcta tcatttggtg gagatgtgac aaagaggttt	1200
ttgcaagata acaatttaga tttgttggtc cggtcacatg aagtaaaaga tgaaggttat	1260
gaggttgaac atgacggtaa actcataact gtcttctctg cgccaaatta ctgtgatcag	1320
atggtaata agggagcctt cattcgaaaa gaagctcctg atatgaagcc aaacattgtt	1380
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aggatgttca actaa	1455

<210> 4
<211> 484
<212> PRT
<213> Arabidopsis thaliana

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35 40 45	
Tyr Trp Ala Asn Arg Ala Phe Ala His Thr Lys Leu Glu Glu Tyr Gly	
50 55 60	
Ser Ala Ile Gln Asp Ala Ser Lys Ala Ile Glu Val Asp Ser Arg Tyr	
65 70 75 80	
Ser Lys Gly Tyr Tyr Arg Arg Gly Ala Ala Tyr Leu Ala Met Gly Lys	
85 90 95	
Phe Lys Asp Ala Leu Lys Asp Phe Gln Gln Val Lys Arg Leu Ser Pro	
100 105 110	
Asn Asp Pro Asp Ala Thr Arg Lys Leu Lys Glu Cys Glu Lys Ala Val	
115 120 125	
Met Lys Leu Lys Phe Glu Glu Ala Ile Ser Val Pro Val Ser Glu Arg	
130 135 140	
Arg Ser Val Ala Glu Ser Ile Asp Phe His Thr Ile Glu Val Glu Pro	
145 150 155 160	

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Gln Tyr Ser Gly Ala Arg Ile Glu Gly Glu Val Thr Leu Asp Phe
 165 170 175
 Val Lys Thr Met Met Glu Asp Phe Lys Asn Gln Lys Thr Leu His Lys
 180 185 190
 Arg Tyr Ala Tyr Gln Ile Val Leu Gln Thr Arg Gln Ile Leu Leu Ala
 195 200 205
 Leu Pro Ser Leu Val Asp Ile Ser Val Pro His Gly Lys His Ile Thr
 210 215 220
 Val Cys Gly Asp Val His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe
 225 230 235 240
 Glu Leu Asn Gly Leu Pro Ser Glu Glu Asn Pro Tyr Leu Phe Asn Gly
 245 250 255
 Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Ile Ile Leu Thr Leu
 260 265 270
 Phe Ala Phe Lys Cys Met Cys Pro Ser Ser Ile Tyr Leu Ala Arg Gly
 275 280 285
 Asn His Glu Ser Lys Ser Met Asn Lys Ile Tyr Gly Phe Glu Gly Glu
 290 295 300
 Val Arg Ser Lys Leu Ser Glu Lys Phe Val Asp Leu Phe Ala Glu Val
 305 310 315 320
 Phe Cys Tyr Leu Pro Leu Ala His Val Ile Asn Gly Lys Val Phe Val
 325 330 335
 Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile
 340 345 350
 Arg Ala Ile Asp Arg Phe Cys Glu Pro Pro Glu Glu Gly Leu Met Cys
 355 360 365
 Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser
 370 375 380
 Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe
 385 390 395 400
 Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys
 405 410 415
 Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe
 420 425 430
 Ser Ala Pro Asn Tyr Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile
 435 440 445
 Arg Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala
 450 455 460
 Val Pro His Pro Asp Val Lys Pro Met Ala Tyr Ala Asn Asn Phe Leu
 465 470 475 480
 Arg Met Phe Asn

<210> 5
 <211> 24
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> PCR primer

<400> 5
ggatccatgg agaccaagaa tgag 24

<210> 6
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 6
ctcgagtttag ttgaacatcc tgag 24

<210> 7
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 7
ggatccgatg tcaggctcta ggccgact 28

<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 8
gctgatcagc atggttccg gagtcggggg tagt 34

<210> 9
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 9
cccgccccga ctaatatggc atcatcagca tcat 34

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

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<400>	10		
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		27	
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<212>	DNA		
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<400>	11		
ggatccatgc	cagtatctga	aaggcgt	
		27	
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<212>	DNA		
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<400>	12		
atggagacca	agaatgagaa	ttct	
		24	
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<212>	DNA		
<213>	Artificial Sequence		
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<400>	13		
ttagttgaac	atcctgagaa	agtt	
		24	
<210>	14		
<211>	347		
<212>	PRT		
<213>	Arabidopsis thaliana		
<400>	14		
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His Thr Ile Glu Val Glu Pro Gln Tyr Ser Gly Ala Arg Ile Glu Gly			
20	25	30	
Glu Glu Val Thr Leu Asp Phe Val Lys Thr Met Met Glu Asp Phe Lys			
35	40	45	
Asn Gln Lys Thr Leu His Lys Arg Tyr Ala Tyr Gln Ile Val Leu Gln			
50	55	60	
Thr Arg Gln Ile Leu Leu Ala Leu Pro Ser Leu Val Asp Ile Ser Val			
65	70	75	80
Pro His Gly Lys His Ile Thr Val Cys Gly Asp Val His Gly Gln Phe			
85	90	95	

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Tyr Asp Leu Leu Asn Ile Phe Glu Leu Asn Gly Leu Pro Ser Glu Glu
 100 105 110

Asn Pro Tyr Leu Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Phe Ser
 115 120 125

Val Glu Ile Ile Leu Thr Leu Phe Ala Phe Lys Cys Met Cys Pro Ser
 130 135 140

Ser Ile Tyr Leu Ala Arg Gly Asn His Glu Ser Lys Ser Met Asn Lys
 145 150 155 160

Ile Tyr Gly Phe Glu Gly Glu Val Arg Ser Lys Leu Ser Glu Lys Phe
 165 170 175

Val Asp Leu Phe Ala Glu Val Phe Cys Tyr Leu Pro Leu Ala His Val
 180 185 190

Ile Asn Gly Lys Val Phe Val Val His Gly Gly Leu Phe Ser Val Asp
 195 200 205

Gly Val Lys Leu Ser Asp Ile Arg Ala Ile Asp Arg Phe Cys Glu Pro
 210 215 220

Pro Glu Glu Gly Leu Met Cys Glu Leu Leu Trp Ser Asp Pro Gln Pro
 225 230 235 240

Leu Pro Gly Arg Gly Pro Ser Lys Arg Gly Val Gly Leu Ser Phe Gly
 245 250 255

Gly Asp Val Thr Lys Arg Phe Leu Gln Asp Asn Asn Leu Asp Leu Leu
 260 265 270

Val Arg Ser His Glu Val Lys Asp Glu Gly Tyr Glu Val Glu His Asp
 275 280 285

Gly Lys Leu Ile Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Gln Met
 290 295 300

Gly Asn Lys Gly Ala Phe Ile Arg Phe Glu Ala Pro Asp Met Lys Pro
 305 310 315 320

Asn Ile Val Thr Phe Ser Ala Val Pro His Pro Asp Val Lys Pro Met
 325 330 335

Ala Tyr Ala Asn Asn Phe Leu Arg Met Phe Asn
 340 345

<210> 15
 <211> 1041
 <212> DNA
 <213> Arabidopsis thaliana

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 gagccacaat attctgggtgc tagaatttagag ggagaggaag ttaccttaga ttttgtgaaa 120
 acgatgatgg aggattttaa gaaccaaaaa acattgcata aacggtatgc ctatcaaatc 180
 gtcttacaga ctaggcaaat cttgctagca ctgccttctc ttgttgatat aagtgttcca 240
 catggcaaac atatcactgt ttgcgggtgac gttcatggtc agttctacga tcttctcaat 300
 atcttgagc ttaatggcct cccttcggag gagaacccat acctattaa tggcgacttt 360

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gtggacagag gctcattctc cgtttagatc atcctactt tgtttgctt caagtgcatt	420
tgcctcatcat ccatatatct agccagagga aaccatgaaa gcaagagcat gaacaaaatt	480
tatggtttg agggtgaggt tcggtccaag ttgagtgaaa aattcgtgga tctcttgct	540
gaagtttctt gttacctccc gttggctcat gttataaatg ggaaggctt cgtggtacat	600
ggaggtcttt tcagtgttga cggcgtgaaa ctctcagaca tcagagccat tgacagattc	660
tgtgagccac cagaggaagg actaatgtgt gaactattgt ggagtgatcc tcaacctctc	720
cctggaagag gcccaagcaa gcgaggagtt ggtcttatcat ttggtgaga tgtgacaaag	780
aggttttgc aagataacaa tttagatttgc ttggccggc cacatgaagt aaaagatgaa	840
ggttatgagg ttgaacatga cggtaaactc ataactgtct tctctgcgcc aaattactgt	900
gatcagatgg gtaataaggg agcatttcatt cgtttgaag ctccgtat gaaagccaaac	960
attgttacat tctcagcagt gcctcatccg gatgtgaagc ctatggcata tgcaaacaac	1020
tttctcagga tggtaacta a	1041

<210> 16
<211> 479
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)
<223> PAPP5

<400> 16
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Lys Ser Gln Ala Asn Glu Ala Phe Lys Gly His Lys Tyr Ser Ser Ala
20 25 30
Ile Asp Leu Tyr Thr Lys Ala Ile Glu Leu Asn Ser Asn Asn Ala Val
35 40 45
Tyr Trp Ala Asn Arg Ala Phe Ala His Thr Lys Leu Glu Glu Tyr Gly
50 55 60
Ser Ala Ile Gln Asp Ala Ser Lys Ala Ile Glu Val Asp Ser Arg Tyr
65 70 75 80
Ser Lys Gly Tyr Tyr Arg Arg Gly Ala Ala Tyr Leu Ala Met Gly Lys
85 90 95
Glu Lys Asp Ala Leu Lys Asp Phe Gln Gln Val Lys Gly Leu Ser Pro
100 105 110
Asn Asp Pro Asp Ala Thr Arg Lys Leu Lys Glu Cys Glu Lys Ala Val
115 120 125
Met Lys Leu Lys Phe Glu Glu Ala Ile Ser Val Pro Val Ser Glu Arg
130 135 140
Arg Ser Val Ala Glu Ser Ile Asp Phe His Thr Ile Glu Val Glu Pro
145 150 155 160
Gln Tyr Ser Gly Ala Arg Ile Glu Gly Glu Val Thr Leu Asp Phe

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165

170

175

Val Lys Thr Met Met Glu Asp Phe Lys Asn Gln Lys Thr Leu His Lys
 180 185 190
 Arg Tyr Ala Tyr Gln Ile Val Leu Gln Thr Arg Gln Ile Leu Leu Ala
 195 200 205
 Leu Pro Ser Leu Val Asp Ile Ser Val Pro His Gly Lys His Ile Thr
 210 215 220
 Val Cys Gly Asp Val His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe
 225 230 235 240
 Glu Asp Asn Gly Leu Pro Ser Glu Glu Asn Pro Tyr Leu Phe Asn Gly
 245 250 255
 Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Ile Ile Leu Thr Leu
 260 265 270
 Phe Ala Glu Lys Cys Met Cys Pro Ser Ser Ile Tyr Leu Ala Arg Gly
 275 280 285
 Asn His Glu Ser Lys Ser Met Asn Lys Ile Tyr Gly Phe Glu Gly Glu
 290 295 300
 Val Arg Ser Lys Leu Ser Glu Lys Phe Val Asp Leu Phe Ala Glu Val
 305 310 315 320
 Phe Cys Tyr Leu Pro Leu Ala His Val Ile Asn Gly Lys Val Phe Val
 325 330 335
 Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile
 340 345 350
 Arg Ala Ile Asp Arg Phe Cys Glu Pro Phe Glu Glu Gly Leu Met Cys
 355 360 365
 Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser
 370 375 380
 Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe
 385 390 395 400
 Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys
 405 410 415
 Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe
 420 425 430
 Ser Ala Pro Asn Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile Arg
 435 440 445
 Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala Val
 450 455 460
 Pro His Pro Met Ala Tyr Ala Asn Asn Phe Ile Arg Met Phe Asn
 465 470 475

<210> 17
 <211> 492
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)

<223> PPS

<400> 17
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 Phe Lys Ala Lys Asp Tyr Glu Asn Ala Ile Lys Phe Tyr Ser Gln Ala
 35 40 45
 Ile Glu Leu Asn Pro Ser Asn Ala Ile Tyr Tyr Gly Asn Arg Ser Leu
 50 55 60
 Ala Tyr Leu Arg Thr Glu Cys Tyr Gly Tyr Ala Leu Gly Asp Ala Thr
 65 70 75 80
 Arg Ala Ile Glu Leu Asp Lys Lys Tyr Ile Lys Gly Tyr Tyr Arg Arg
 85 90 95
 Ala Ala Ser Asn Met Ala Leu Gly Lys Phe Arg Ala Ala Leu Arg Asp
 100 105 110
 Tyr Glu Thr Val Val Lys Val Lys Pro His Asp Lys Asp Ala Lys Met
 115 120 125
 Lys Tyr Gln Glu Cys Asn Lys Thr Val Lys Gln Lys Ala Phe Glu Arg
 130 135 140
 Ala Ile Gly Asp Glu His Lys Arg Ser Val Val Asp Ser Leu Asp Ile
 145 150 155 160
 Glu Ser Met Thr Ile Glu Asp Glu Tyr Ser Gly Pro Lys Leu Glu Asp
 165 170 175
 Gly Lys Val Thr Ile Ser Phe Met Lys Glu Leu Met Gln Trp Tyr Lys
 180 185 190
 Asp Gln Lys Lys Leu His Arg Lys Cys Ala Tyr Gln Ile Leu Val Gln
 195 200 205
 Val Lys Glu Val Leu Ser Lys Leu Ser Thr Leu Val Glu Thr Thr Leu
 210 215 220
 Lys Glu Thr Glu Lys Ile Thr Val Cys Gly Asp Thr His Gly Gln Phe
 225 230 235 240
 Tyr Asp Leu Leu Asn Ile Phe Glu Leu Asn Gly Leu Pro Ser Glu Thr
 245 250 255
 Asn Pro Tyr Asp Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Phe Ser
 260 265 270
 Val Glu Val Ile Leu Thr Leu Phe Gly Phe Lys Leu Leu Tyr Pro Asp
 275 280 285
 His Phe His Leu Leu Arg Gly Asn His Glu Thr Asp Asn Met Asn Gln
 290 295 300
 Ile Tyr Gly Phe Glu Gly Glu Val Lys Ala Lys Tyr Thr Ala Gln Met
 305 310 315 320
 Tyr Glu Leu Phe Ser Glu Val Phe Glu Trp Leu Pro Leu Ala Gln Cys
 325 330 335
 Ile Asn Gly Lys Val Leu Ile Met His Gly Gly Leu Phe Ser Glu Asp

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340 345 350

Gly Val Thr Leu Asp Asp Ile Arg Lys Ile Glu Arg Asn Arg Gln Pro
355 360 365
Phe Asp Ser Gly Pro Met Cys Asp Leu Leu Trp Ser Asp Pro Gln Pro
370 375 380
Gln Asn Gly Arg Ser Ile Ser Lys Arg Gly Val Ser Cys Gln Phe Gly
385 390 395 400
Pro Asp Val Thr Lys Ala Phe Leu Glu Glu Asn Asn Leu Asp Tyr Ile
405 410 415
Ile Arg Ser His Glu Val Lys Ala Glu Gly Tyr Glu Val Ala His Gly
420 425 430
Gly Arg Cys Val Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Gln Met
435 440 445
Gly Asn Lys Ala Ser Tyr Ile His Leu Gln Gly Ser Asp Leu Arg Pro
450 455 460
Gln Phe His Gln Phe Thr Ala Val Pro His Pro Asn Val Lys Pro Met
465 470 475 480
Ala Tyr Ala Asn Thr Leu Leu Gln Leu Gly Met Met
485 490

<210> 18
<211> 500
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)
<223> PP5

<400> 18
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Asp Glu Pro Pro Ala Asp Gly Leu Ala Lys Arg Ala Glu Glu Leu Lys
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Thr Gln Ala Asn Asp Tyr Phe Lys Ala Lys Asp Tyr Glu Asn Ala Ile
35 40 45
Lys Phe Tyr Ser Gln Ala Ile Glu Leu Asn Pro Gly Asn Ala Ile Tyr
50 55 60
Tyr Gly Asn Arg Ser Leu Ala Tyr Leu Arg Thr Glu Cys Tyr Gly Tyr
65 70 75 80
Ala Leu Gly Asp Ala Thr Arg Ala Ile Glu Leu Asp Lys Lys Tyr Ile
85 90 95
Lys Gly Tyr Tyr Arg Arg Ala Ala Ser Asn Met Ala Leu Gly Lys Phe
100 105 110
Arg Ala Ala Leu Arg Asp Tyr Glu Thr Val Val Lys Val Lys Pro Asn
115 120 125
Asp Lys Asp Ala Lys Met Lys Tyr Gln Glu Cys Ser Lys Thr Val Lys
130 135 140

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Gln Lys Ala Phe Glu Arg Ala Ile Ala Gly Asp Glu His Arg Arg Ser
145 150 155 160
Val Val Asp Ser Leu Asp Ile Glu Ser Met Thr Ile Glu Asp Glu Tyr
165 170 175
Ser Gly Pro Lys Leu Glu Asp Gly Lys Val Thr Ile Thr Phe Met Lys
180 185 190
Asp Leu Met Gln Trp Tyr Lys Asp Gln Lys Lys Leu His Arg Lys Cys
195 200 205
Ala Tyr Gln Ile Leu Val Gln Val Lys Glu Val Leu Cys Lys Leu Ser
210 215 220
Thr Leu Val Glu Thr Thr Leu Lys Glu Thr Glu Lys Ile Thr Val Cys
225 230 235 240
Gly Asp Thr His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe Glu Leu
245 250 255
Asn Gly Leu Pro Ser Glu Thr Thr Asn Pro Tyr Thr Phe Asn Gly Asp
260 265 270
Phe Val Asp Arg Gly Ser Phe Ser Val Glu Val Ile Leu Thr Leu Phe
275 280 285
Gly Phe Lys Leu Leu Tyr Pro Asp His Phe His Leu Leu Arg Gly Asn
290 295 300
His Glu Thr Asp Asn Met Asn Gln Ile Tyr Gly Phe Glu Gly Glu Val
305 310 315 320
Lys Ala Lys Tyr Thr Ala Gln Met Tyr Glu Leu Phe Ser Glu Val Glu
325 330 335
Glu Trp Leu Pro Leu Ala Gln Cys Ile Asn Gly Lys Val Leu Ile Met
340 345 350
His Gly Gly Leu Phe Ser Glu Asp Gly Val Thr Leu Asp Asp Ile Arg
355 360 365
Lys Ile Glu Arg Asn Arg Gln Pro Pro Asp Ser Gly Pro Met Cys Asp
370 375 380
Leu Leu Trp Ser Asp Pro Gln Pro Gln Asn Gly Arg Ser Val Ser Lys
385 390 395 400
Arg Gly Val Ser Cys Gln Phe Gly Pro Asp Val Thr Lys Ala Phe Leu
405 410 415
Glu Glu Asn Gln Leu Asp Tyr Ile Ile Arg Ser His Glu Val Lys Ala
420 425 430
Glu Gly Tyr Glu Val Ala His Gly Gly Arg Cys Val Thr Val Phe Ser
435 440 445
Ala Pro Asn Tyr Cys Asp Gln Met Gly Asn Lys Ala Ser Tyr Ile His
450 455 460
Leu Gln Gly Ser Asp Leu Arg Pro Gln Phe His Gln Phe Thr Ala Val
465 470 475 480
Pro His Pro Asn Val Lys Pro Met Ala Tyr Ala Asn Thr Leu Leu Gln
485 490 495
Leu Gly Met Met

<210> 19
<211> 497
<212> PRT
<213> Rattus norvegicus

<220>
<221> PEPTIDE
<222> (1)
<223> PP5

<400> 19
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20 25 30
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35 40 45
Lys Phe Tyr Ser Gln Ala Ile Glu Leu Asn Pro Ser Asn Ala Ile Tyr 60
50 55 60
Tyr Gly Asn Arg Ser Leu Ala Tyr Leu Arg Thr Glu Cys Tyr Gly Tyr 80
65 70 75 80
Ala Leu Gly Asp Ala Thr Arg Ala Ile Glu Leu Asp Lys Lys Tyr Ile 95
85 90 95
Lys Gly Tyr Tyr Arg Arg Ala Ala Ser Asn Met Ala Leu Gly Lys Phe 110
100 105 110
Arg Ala Ala Leu Arg Asp Tyr Glu Thr Val Val Lys Pro Asn Asp Lys 125
115 120 125
Asp Ala Lys Met Lys Tyr Gln Glu Cys Ser Lys Thr Val Lys Gln Lys 140
130 135 140
Gln Phe Glu Arg Ala Ile Ala Gly Asp Glu His Arg Arg Ser Val Val 160
145 150 155 160
Asp Ser Leu Asp Ile Glu Ser Met Thr Leu Glu Asp Glu Tyr Ser Gly 175
165 170 175
Pro Lys Leu Glu Asp Gly Lys Val Thr Ile Thr Phe Met Lys Asp Leu 190
180 185 190
Met Gln Trp Tyr Lys Asp Gln Lys Lys Leu His Arg Lys Cys Ala Tyr 205
195 200 205
Gln Ile Leu Val Gln Val Lys Glu Val Leu Val Lys Leu Ser Thr Leu 220
210 215 220
Val Glu Thr Thr Leu Lys Glu Thr Glu Lys Ile Thr Val Cys Gly Asp 240
225 230 235 240
Thr His Gly Gln Phe Tyr Asp Leu Leu Asn Glu Phe Glu Leu Asn Gly 255
245 250 255
Leu Pro Ser Glu Thr Asn Pro Tyr Ile Glu Asn Gly Asp Phe Val Asp 270
260 265 270
Arg Gly Ser Phe Ser Val Glu Val Ile Leu Thr Leu Phe Gly Phe Lys 285
275 280 285

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Leu Leu Tyr Pro Asp His Phe His Leu Leu Arg Gly Asn His Glu Thr
290 295 300
Asp Asn Met Asn Gln Ile Tyr Gly Phe Glu Gly Glu Val Lys Ala Lys
305 310 315 320
Tyr Thr Ala Gln Met Tyr Glu Leu Phe Ser Glu Val Glu Glu Trp Leu
325 330 335
Pro Leu Ala Gln Cys Ile Asn Gly Lys Val Leu Ile Met His Gly Gly
340 345 350
Leu Phe Ser Glu Asp Gly Val Thr Leu Asp Asp Ile Pro Lys Ile Glu
355 360 365
Arg Asn Arg Gln Pro Phe Asp Ser Gly Pro Met Cys Asp Leu Leu Trp
370 375 380
Ser Asp Pro Gln Pro Gln Asn Gly Arg Ser Val Ser Lys Arg Gly Val
385 390 395 400
Ser Cys Gln Phe Gly Pro Asp Val Thr Lys Ala Phe Leu Glu Glu Asn
405 410 415
Gln Leu Asp Tyr Ile Ile Arg Ser His Glu Val Lys Ala Glu Gly Tyr
420 425 430
Glu Val Ala His Gly Gly Arg Cys Val Thr Val Phe Ser Ala Pro Asn
435 440 445
Tyr Cys Asp Gln Met Gly Asn Lys Ala Ser Tyr Ile His Leu Gln Gly
450 455 460
Ser Asp Leu Arg Pro Gln Phe His Gln Phe Thr Ala Val Pro His Pro
465 470 475 480
Asn Val Lys Pro Met Ala Tyr Ala Asn Ile Leu Leu Gln Leu Gly Met
485 490 495
Met

<210> 20
<211> 513
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> PEPTIDE
<222> (1)
<223> PP5

<400> 20
Met Ser Thr Pro Thr Ala Ala Asp Arg Ala Lys Ala Leu Glu Arg Lys
1 5 10 15
Asn Glu Gly Asn Val Phe Val Lys Glu Lys His Phe Leu Lys Ala Ile
20 25 30
Glu Lys Tyr Thr Glu Ala Ile Asp Leu Asp Ser Thr Gln Ser Ile Tyr
35 40 45
Phe Ser Asn Arg Ala Phe Ala His Phe Lys Val Asp Asn Phe Gln Ser
50 55 60

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Ala Leu Asn Asp Cys Asp Glu Ala Ile Lys Leu Asp Pro Lys Asn Ile
 65 70 75 80

Lys Ala Tyr His Arg Arg Ala Leu Ser Cys Met Ala Leu Leu Glu Glu
 85 90 95

Lys Lys Ala Arg Lys Asp Leu Asn Val Leu Leu Lys Ala Lys Pro Asn
 100 105 110

Asp Pro Ala Ala Thr Lys Ala Leu Leu Thr Cys Asp Arg Phe Ile Arg
 115 120 125

Glu Glu Arg Phe Arg Lys Ala Ile Gly Gly Ala Glu Asn Glu Ala Lys
 130 135 140

Ile Ser Leu Cys Gln Thr Leu Asn Leu Ser Ser Phe Asp Ala Asn Ala
 145 150 155 160

Asp Leu Ala Asn Tyr Glu Gly Pro Lys Leu Glu Phe Glu Gln Leu Tyr
 165 170 175

Asp Asp Lys Asn Ala Phe Lys Gly Ala Lys Ile Lys Asn Met Ser Gln
 180 185 190

Glu Phe Ile Ser Lys Met Val Asn Asp Leu Phe Leu Lys Gly Lys Tyr
 195 200 205

Leu Pro Lys Lys Tyr Val Ala Ala Ile Thr Ser His Ala Asp Thr Leu
 210 215 220

Phe Arg Gln Glu Pro Ser Met Val Glu Leu Glu Asn Asn Ser Thr Pro
 225 230 235 240

Asp Val Lys Ile Ser Val Cys Gly Asp Thr His Gly Gln Phe Tyr Asp
 245 250 255

Val Leu Asn Leu Phe Arg Lys Phe Gly Lys Val Gly Pro Lys His Thr
 260 265 270

Tyr Leu Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Trp Ser Cys Glu
 275 280 285

Val Ala Leu Leu Phe Tyr Cys Leu Lys Ile Leu His Pro Asn Asn Phe
 290 295 300

Phe Leu Asn Arg Gly Asn His Glu Ser Asp Asn Met Asn Lys Ile Tyr
 305 310 315 320

Gly Phe Glu Asp Glu Cys Lys Tyr Lys Tyr Ser Gln Arg Thr Phe Asn
 325 330 335

Met Phe Ala Gln Ser Phe Glu Ser Leu Pro Leu Ala Thr Leu Ile Asn
 340 345 350

Asn Asp Tyr Leu Val Met His Gly Gly Leu Pro Ser Asp Pro Ser Ala
 355 360 365

Thr Leu Ser Asp Phe Lys Asn Ile Asp Arg Phe Ala Gln Pro Pro Arg
 370 375 380

Asp Gly Ala Phe Met Glu Leu Leu Trp Ala Asp Pro Gln Glu Ala Asn
 385 390 395 400

Gly Met Gly Pro Ser Gln Arg Gly Leu Gly His Ala Phe Gly Pro Asp
 405 410 415

Ile Thr Asp Arg Phe Leu Arg Asn Asn Lys Leu Arg Lys Ile Phe Arg
 420 425 430

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Ser His Glu Leu Arg Met Gly Gly Val Gln Phe Glu Gln Lys Gly Lys
435 440 445
Leu Met Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Ser Gln Gly Asn
450 455 460
Leu Gly Gly Val Ile His Val Val Pro Gly His Gly Ile Leu Gln Ala
465 470 475 480
Gly Arg Asn Asp Asp Gln Asn Leu Ile Ile Glu Thr Phe Glu Ala Val
485 490 495
Glu His Pro Asp Ile Lys Pro Met Ala Tyr Ser Asn Gly Gly Phe Gly
500 505 510
Leu

<210> 21
<211> 520
<212> PRT
<213> Drosophila melanogaster

<220>
<221> PEPTIDE
<222> (1)
<223> PP5

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Glu Ala Lys Val Pro Ala Ser Val Glu Ile Thr Gly Ser Lys Gln Pro
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Glu Glu Asp Thr Asn Ala Arg Thr Lys Ala Glu Leu Asp Phe Ala Ala
35 40 45
Ala Glu Gln Tyr Lys Asn Gln Gly Asn Glu Met Leu Lys Thr Lys Glu
50 55 60
Phe Ser Lys Ala Ile Asp Met Tyr Thr Lys Ala Leu Glu Leu His Pro
65 70 75 80
Asn Ser Ala Ile Tyr Tyr Ala Asn Arg Ser Leu Ala His Leu Arg Gln
85 90 95
Glu Ser Phe Gly Phe Ala Leu Gln Asp Gly Val Ser Ala Val Lys Ala
100 105 110
Asp Pro Ala Tyr Leu Lys Gly Tyr Tyr Arg Arg Ala Ala Ala His Met
115 120 125
Ser Leu Gly Lys Phe Lys Gln Ala Leu Cys Asp Phe Glu Phe Val Ala
130 135 140
Lys Cys Arg Pro Asn Asp Lys Asp Ala Lys Ile Lys Phe Thr Glu Cys
145 150 155 160
Asn Lys Thr Val Lys Met Arg Ala Phe Glu Arg Ala Ile Ala Val Asp
165 170 175
Lys Pro Glu Lys Thr Leu Ser Glu Met Tyr Ser Asp Met Glu Asn Ile
180 185 190

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Thr Ile Glu Asp Asp Tyr Lys Gly Pro Gln Leu Glu Asp Gly Lys Val
 195 200 205
 Thr Leu Lys Phe Met Lys Glu Leu Met Glu His Thr Lys Ala Gln Lys
 210 215 220
 Arg Leu His Arg Lys Phe Ala Tyr Lys Ile Leu Cys Glu Ile Asp Thr
 225 230 235 240
 Tyr Met Arg Ala Gln Pro Ser Leu Val Asp Ile Thr Val Pro Asp Glu
 245 250 255
 Glu Lys Glu Thr Ile Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu
 260 265 270
 Met Asn Ile Phe Glu Ile Asn Gly Leu Pro Ser Glu Lys Asn Pro Tyr
 275 280 285
 Leu Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Cys
 290 295 300
 Ile Glu Thr Leu Phe Gly Phe Lys Leu Leu Tyr Pro Asn His Phe Phe
 305 310 315 320
 Leu Ala Arg Gly Asn His Glu Ser Ile Asn Met Asn Gln Met Tyr Gly
 325 330 335
 Glu Thr Gly Glu Val Thr Ala Lys Tyr Thr Ser Ala Met Ala Asp Ile
 340 345 350
 Phe Thr Gln Val Glu Asn Trp Leu Pro Leu Cys His Cys Ile Asn Gln
 355 360 365
 Lys Ile Leu Val Met His Gly Gly Leu Phe Ser Thr Glu Asp Val Thr
 370 375 380
 Leu Asp His Ile Arg Arg Ile Glu Arg Asn Cys Gln Pro Pro Glu Glu
 385 390 395 400
 Gly Leu Met Cys Glu Leu Leu Trp Ser Asp Pro Gln Gln Trp Met Gly
 405 410 415
 Leu Gly Gln Ser Lys Arg Gly Val Gly Ile Gln Phe Gly Pro Asp Val
 420 425 430
 Thr Glu Lys Glu Cys Lys Asp Asn Asn Leu Asp Tyr Ile Ile Arg Ser
 435 440 445
 His Glu Val Lys Asp Met Gly Tyr Glu Val Ala His Asn Gly Lys Cys
 450 455 460
 Ile Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Thr Met Gly Asn Met
 465 470 475 480
 Gly Ala Phe Ile Thr Ile Thr Gly Asn Asn Leu Lys Pro Asn Tyr Lys
 485 490 495
 Ser Phe Glu Ala Val Pro His Pro Asp Val Lys Pro Met Ala Tyr Ala
 500 505 510
 Asn Ser Leu Met Asn Trp Leu Ala
 515 520

<210> 22
 <211> 524
 <212> PRT
 <213> Caenorhabditis elegans

<220>
<221> PEPTIDE
<222> (1)
<223> PP5

<400> 22
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Ile Glu Glu Lys Ser Tyr Glu Asp Glu Lys Glu Lys Ala Gly Met Ile
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Lys Asp Glu Ala Asn Gln Phe Phe Lys Asp Gln Val Tyr Asp Val Ala
35 40 45
Ala Asp Leu Tyr Ser Val Ala Ile Glu Ile His Pro Thr Ala Val Leu
50 55 60
Tyr Gly Asn Arg Ala Gln Ala Tyr Leu Lys Lys Glu Leu Tyr Gly Ser
65 70 75 80
Ala Leu Asp Asp Ala Asp Asn Ala Ile Ala Ile Asp Pro Ser Tyr Val
85 90 95
Lys Gly Phe Tyr Arg Arg Ala Thr Ala Asn Met Ala Leu Gly Arg Phe
100 105 110
Lys Lys Ala Leu Thr Asp Tyr Gln Ala Val Val Lys Val Cys Pro Asn
115 120 125
Asp Lys Asp Ala Arg Ala Lys Phe Asp Glu Cys Ser Lys Ile Val Arg
130 135 140
Arg Gln Lys Phe Glu Ala Ala Ile Ser Thr Asp His Asp Lys Lys Thr
145 150 155 160
Val Ala Glu Thr Leu Asp Ile Asn Met Ala Ile Glu Asp Ser Tyr Asp
165 170 175
Gly Pro Arg Leu Glu Asp Lys Ile Thr Lys Glu Phe Val Leu Gln Leu
180 185 190
Ile Lys Thr Phe Lys Asn Gln Gln Lys Leu His Lys Lys Tyr Ala Phe
195 200 205
Lys Met Leu Leu Glu Phe Tyr Asn Tyr Val Lys Ser Leu Pro Thr Met
210 215 220
Val Glu Ile Thr Val Pro Thr Gly Lys Lys Phe Thr Ile Cys Gly Asp
225 230 235 240
Val His Gly Gln Phe Tyr Asp Leu Cys Asn Ile Phe Glu Ile Asn Gly
245 250 255
Tyr Pro Ser Glu Thr Asn Pro Tyr Leu Phe Asn Gly Asp Phe Val Asp
260 265 270
Arg Gly Ser Phe Ser Val Glu Thr Ile Phe Thr Met Ile Gly Phe Lys
275 280 285
Leu Leu Pro Asn His Phe Phe Met Ser Arg Gly Asn His Glu Ser Asp
290 295 300
Val Met Asn Lys Met Tyr Gly Phe Glu Gly Glu Val Lys Ala Lys Tyr
305 310 315 320

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Thr	Gln	Gln	Met	Cys	Asp	Met	Phe	Thr	Glu	Thr	Phe	Cys	Trp	Leu	Pro
			325					330					335		
Leu	Cys	His	Leu	Ile	Asn	Glu	Lys	Ile	Phe	Val	cys	His	Gly	Gly	Leu
	340						345					350			
Phe	Lys	Glu	Asp	Gly	Val	Thr	Leu	Glu	Asp	Ile	Arg	Lys	Thr	Asp	Arg
	355						360					365			
Asn	Arg	Gln	Pro	Pro	Asp	Glu	Gly	Ile	Met	Cys	Asp	Leu	Leu	Trp	Glu
	370					375						380			
Lys	Asn	Trp	Lys	Asn	Leu	Lys	Ile	Leu	Tyr	Pro	Asp	Gly	Lys	Ile	Asn
	385				390				395				400		
Lys	Asn	Ser	Asn	Cys	Gln	Pro	Lys	Thr	Cys	Lys	Asn	Ala	Ser	Asp	Pro
	405							410					415		
Gln	Pro	Ile	Asn	Gly	Arg	Ser	Pro	Ser	Lys	Arg	Gly	Val	Gly	Cys	Gln
	420							425					430		
Phe	Gly	Pro	Asp	Val	Thr	Ser	Lys	Trp	Cys	Glu	Thr	Asn	Gly	Ile	Glu
	435							440					445		
Tyr	Val	Val	Arg	Ser	His	Glu	Val	Lys	Pro	Glu	Gly	Tyr	Glu	Met	His
	450					455						460			
His	Asn	Gly	Gln	Cys	Phe	Thr	Val	Phe	Ser	Ala	Pro	Asn	Tyr	Cys	Asp
	465					470						475			480
Gln	Met	Asn	Asn	Lys	Gly	Ala	Phe	Ile	Thr	Ile	Thr	Gly	Asp	Asn	Leu
	485							490					495		
Thr	Pro	Arg	Phe	Thr	Pro	Phe	Asp	Ala	Val	Pro	His	Pro	Lys	Leu	Pro
	500							505					510		
Pro	Met	Ala	Tyr	Ala	Asn	Ser	Leu	Phe	Gly	Phe	Asn				
	515							520							

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<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> PP2A motif

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<221> misc_feature
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<400> 23
Gly Asp Xaa His Gly Gln
1 5

<210> 24
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> PP2A motif

<220>
<221> misc_feature

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<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid

<400> 24
Gly Asp Xaa Val Xaa Arg Gly
1 5

<210> 25
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> PP2A motif

<400> 25
Arg Gly Asn His Glu
1 5

<210> 26
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> C-terminal consensus sequence

<400> 26
Ser Ala Pro Asn Tyr Cys
1 5